

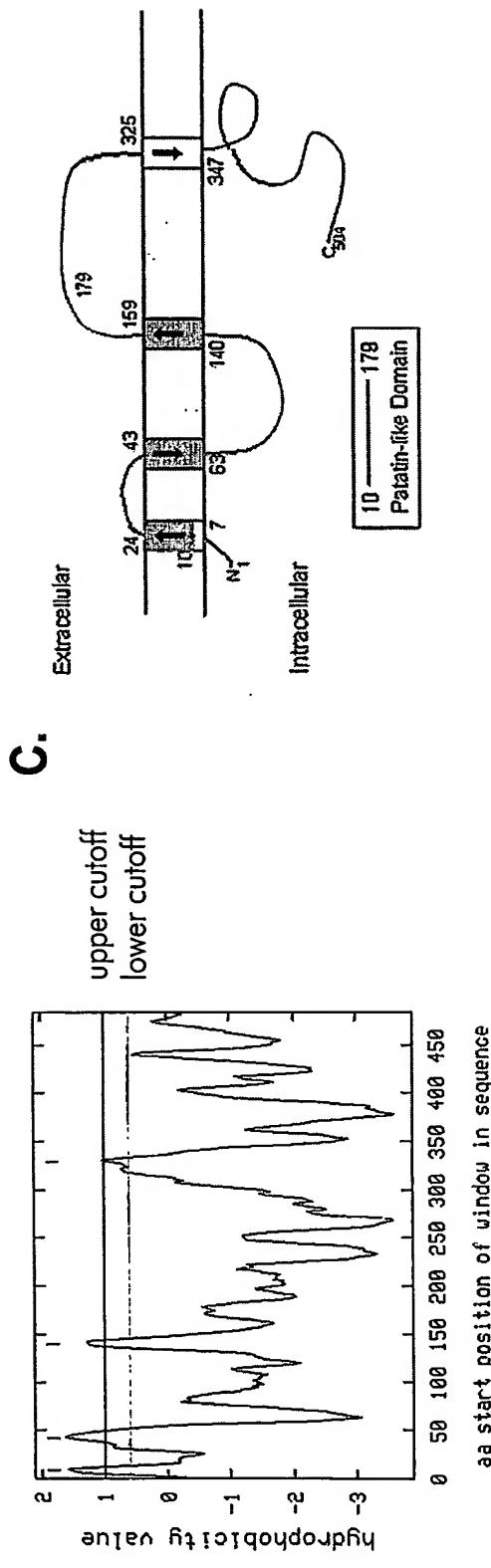
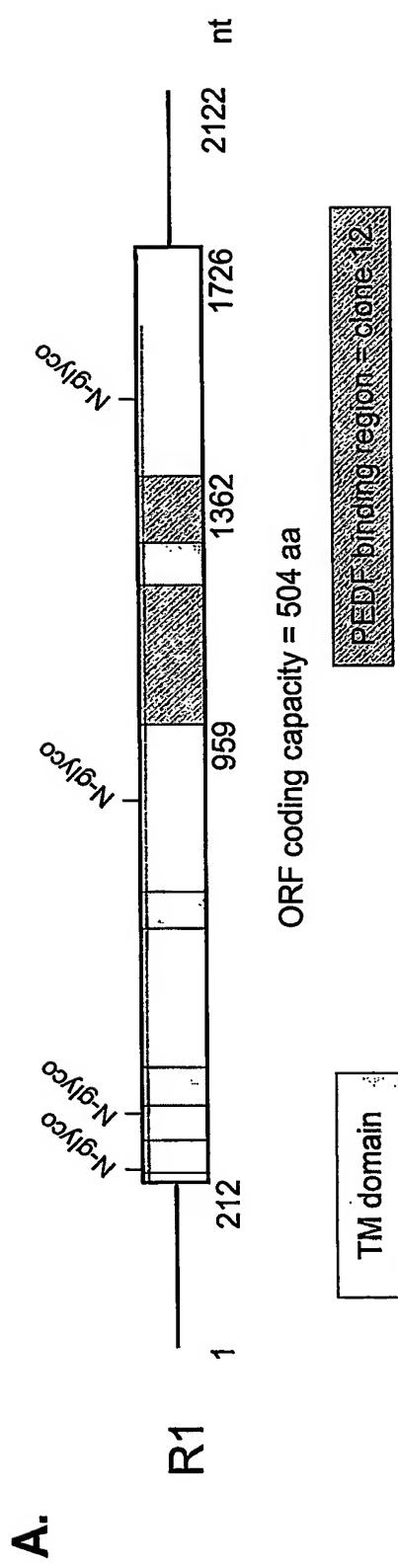
Figure 1.**BEST AVAILABLE COPY**

Figure 1.
D.

R1 adiponutrin	MFPREKTIWNISFAGGCCFLGVVYVGGASCLREHAPPFLVANATHIYGASAGALLATAVVGVLGEA YDA RG SL F H ATR H LRD RMLF HCVGVLSI I P EQTLQVLSDLVRK S NI
PLHPSEFMNLVKIIRSFLLKVLPADSEHEHASGRGLGISLTVSDGENVITISHFNNSKDELIOANVCNSGFGFIPVYCGNIPPSLQG IF S FL QG C C NV QLI KI LV DFR VVD L C F S FR	
DGGISDNLPLXELKNTIVSPFSGESDICPQDSSTNIHELRVTNTSIQFNRLNLYRLSKA LFPPPEPLVREMCKQGYRDGLR V V FIDA T P Y Y KVK FLHVDI KL LRLCTG L R FV DLK G I LR L AF	
FLQRNGLLNRNP-LLAIPP-----ARPHEGPEDKDOAVESAQAE--DYSQQLP--GEDH-TLEHILPARLINEALLE EEK IC Q G KSSSEGMDPEVAMPSWANMSLDSS SAAL RLEGD LL HLR SILPW ES DT SP AT S	
ACVEPTDLTLTTSNNLIPVRLATAM\NPYTLPPLSALSFTIRLLEWLPDVPEDIRWMKEQT GSICQ YLVMRAKRKLGRHLPS EMKDKGGMMSKIC L I IMSYV L C V LAIVQ VT M D VL LQWV SQVFTRL CLLPASRSQM V	
RLPEQVELRRVQSLPS-VPLSCAAVREALPGWMRNNNLSLGDALAKWEECQRQLLGLFCTNVAFFPEALMRAPADPAPAPAD SSQQASPCTPE DW CWT C PKGCPAETKAATPRSI RSS NFEIGNKVPGAGAEGIS --- SES EKSU-----	
PASPOHQLAGPAPLLSTPAPEARPVIGALGL -----	
E.	
253 450	GLINRPN PLLALPPARP HGEPKDKDQAV ESAQAEDYSQ LPGE 293 T NVAFPPEALR MRAPADPAPA PADPASPOHQ LAGPAPLLST PAPEARPVIG ALGL 504

Figure 1.
F.

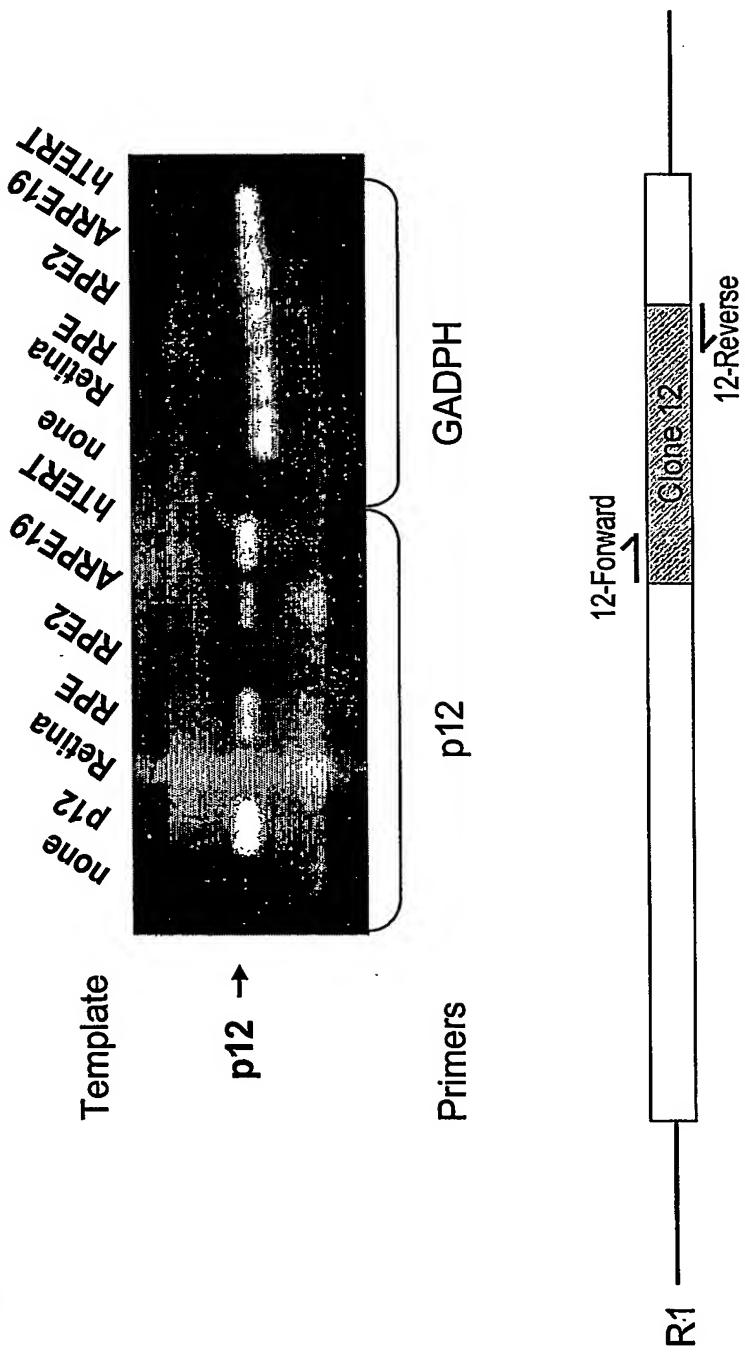
Homologous patatin phospholipase A (PLA) active site in R1: S47 and D166

Active site serine

NA	THIYGASAGA	LTA	R1
YF	DVIGGT S TGG	LLT	Patatain B2
CA	TYVAGL S GST	WYM	cPLA2

Active site aspartic

SLQ	GVRYY D GGGIS	DNLPLYE	R1
ARY	EFNLI V DGAVA	TVGDPAL	Patatin B2
KSK	KIHVV D SGI-	TFNLYP	cPLA2

Figure 2.

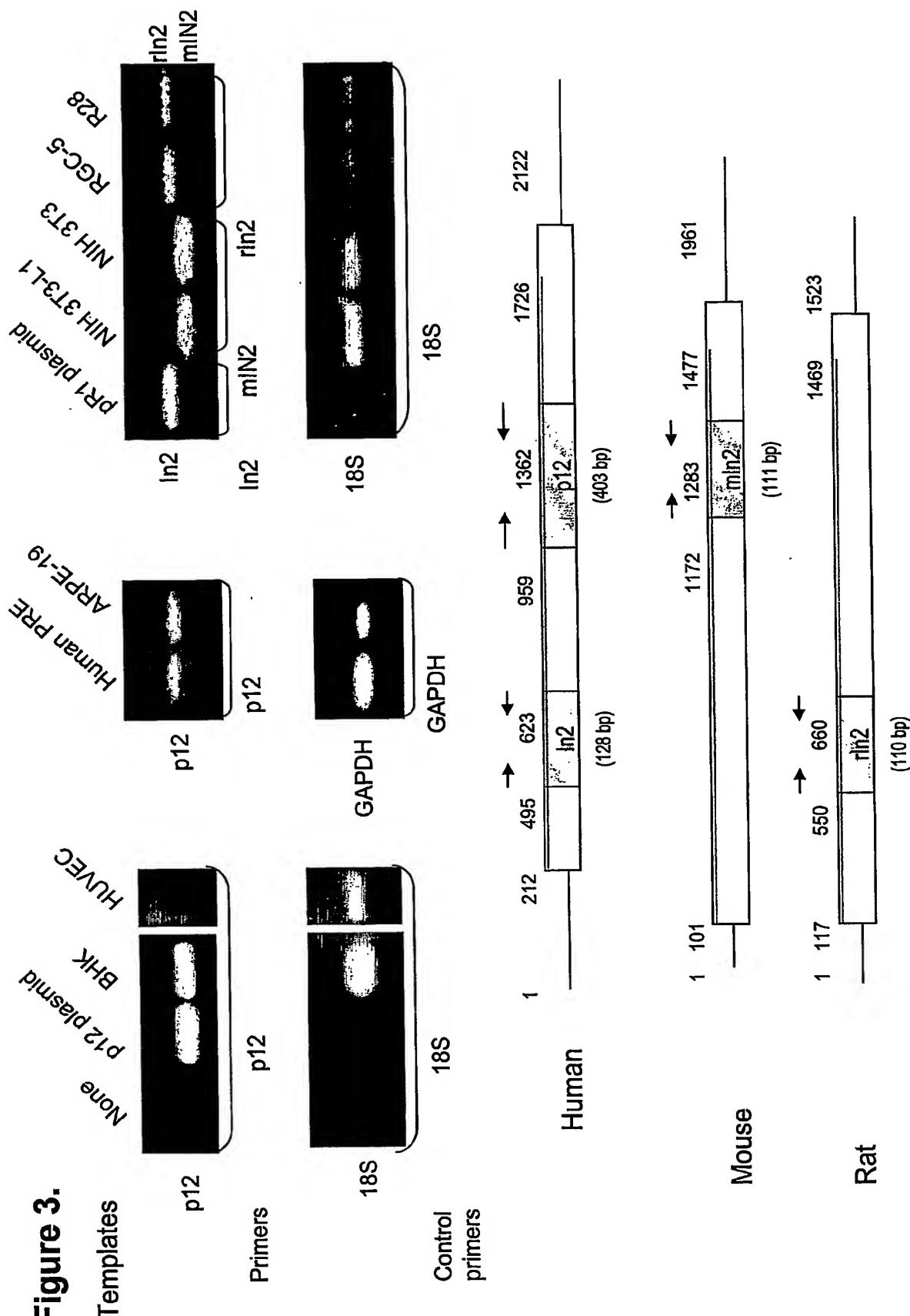
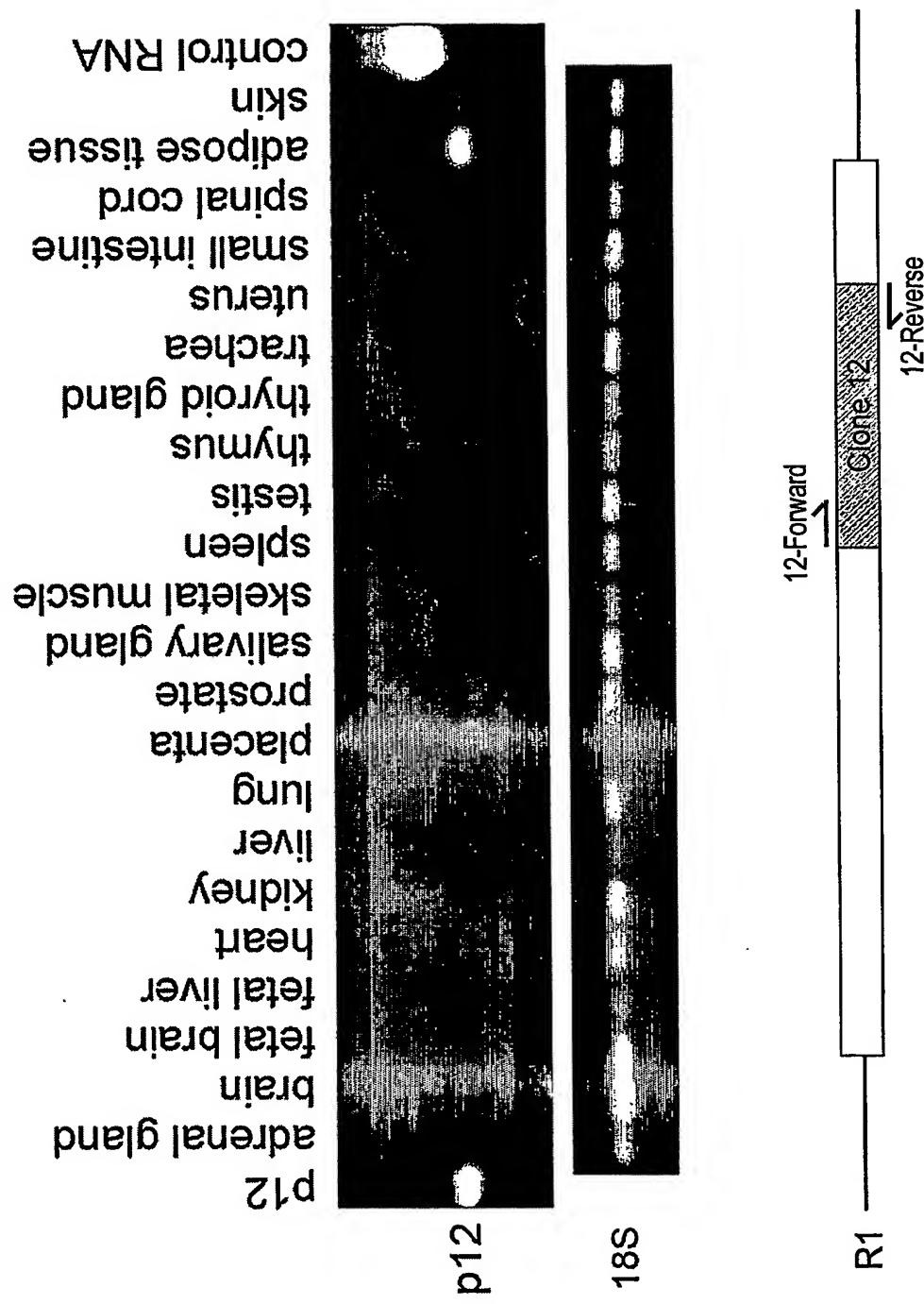


Figure 4.

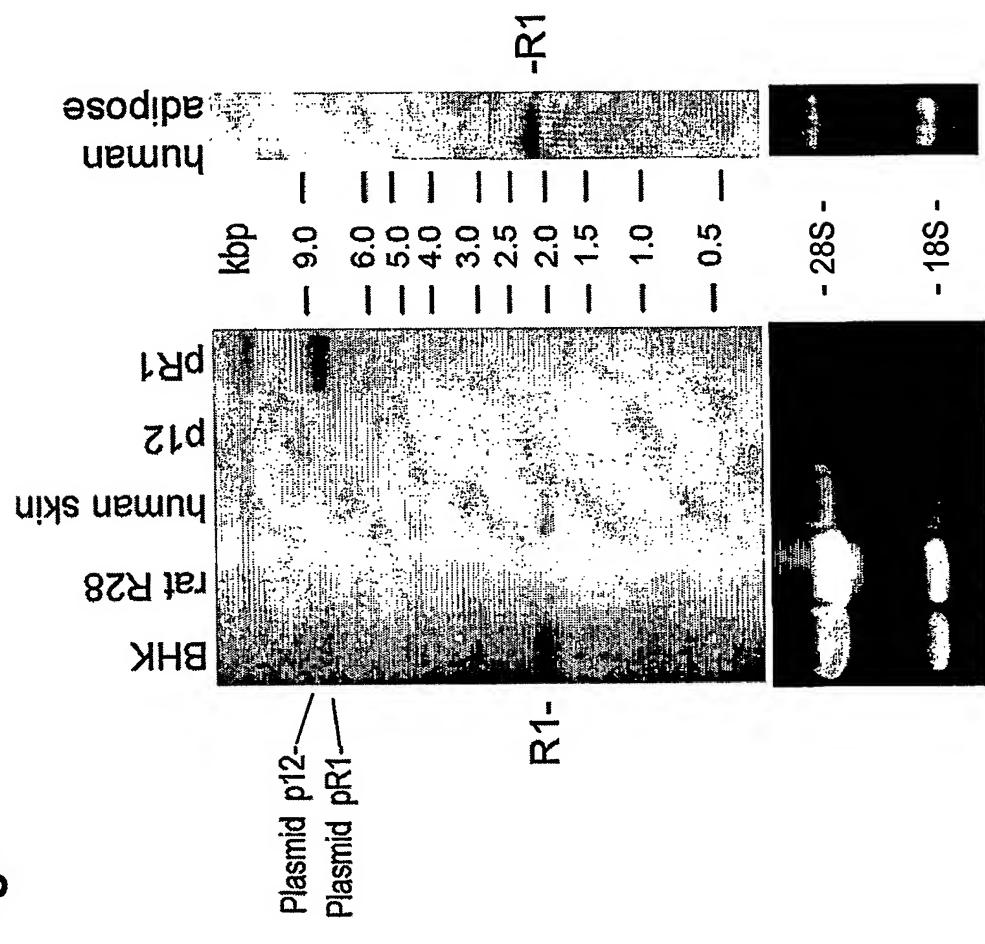


Figure 5.

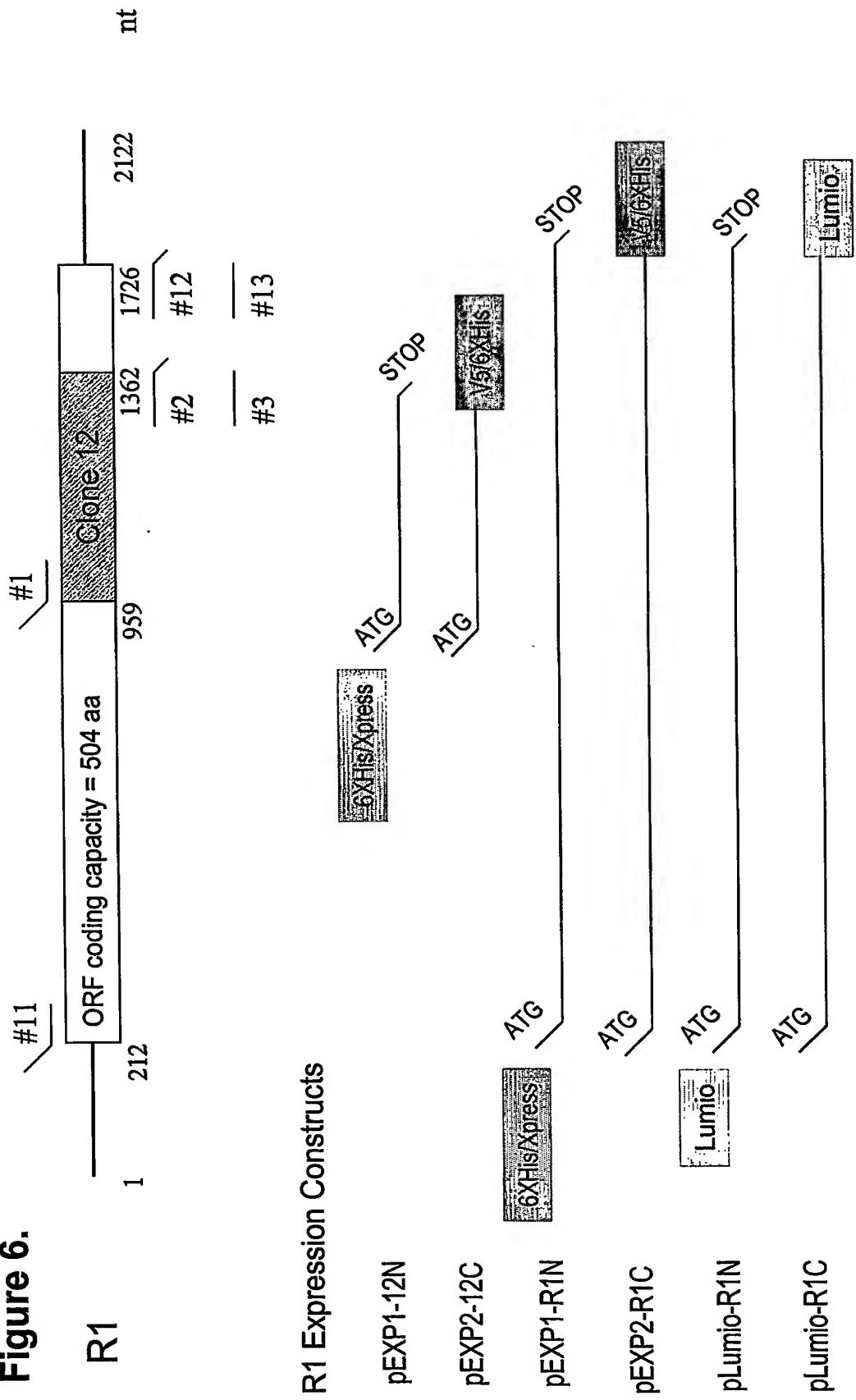
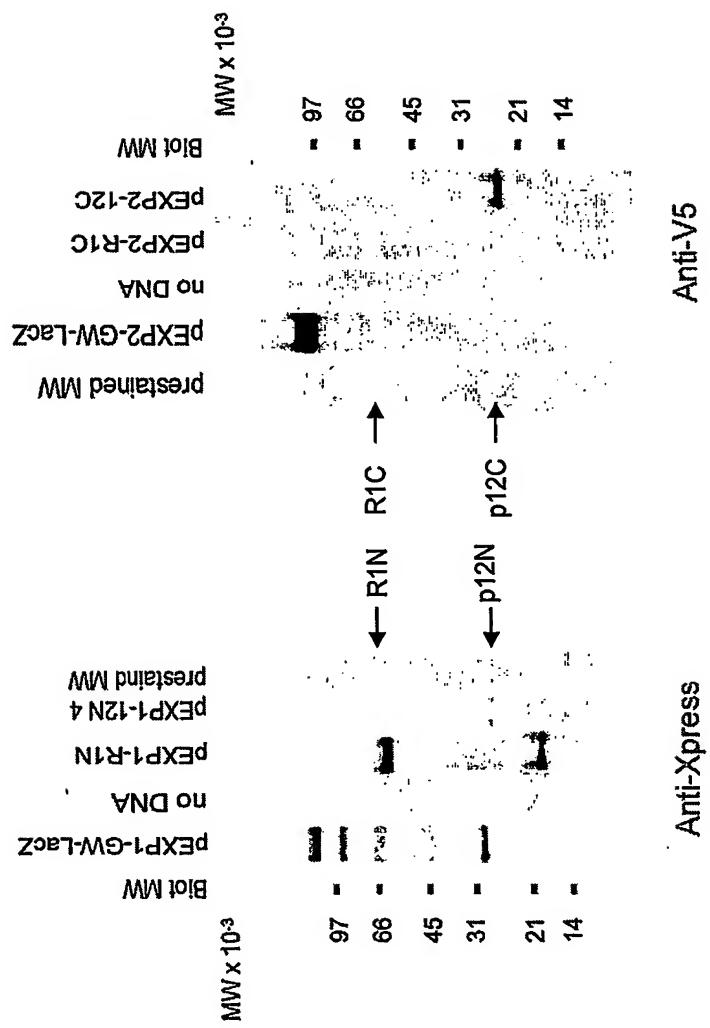
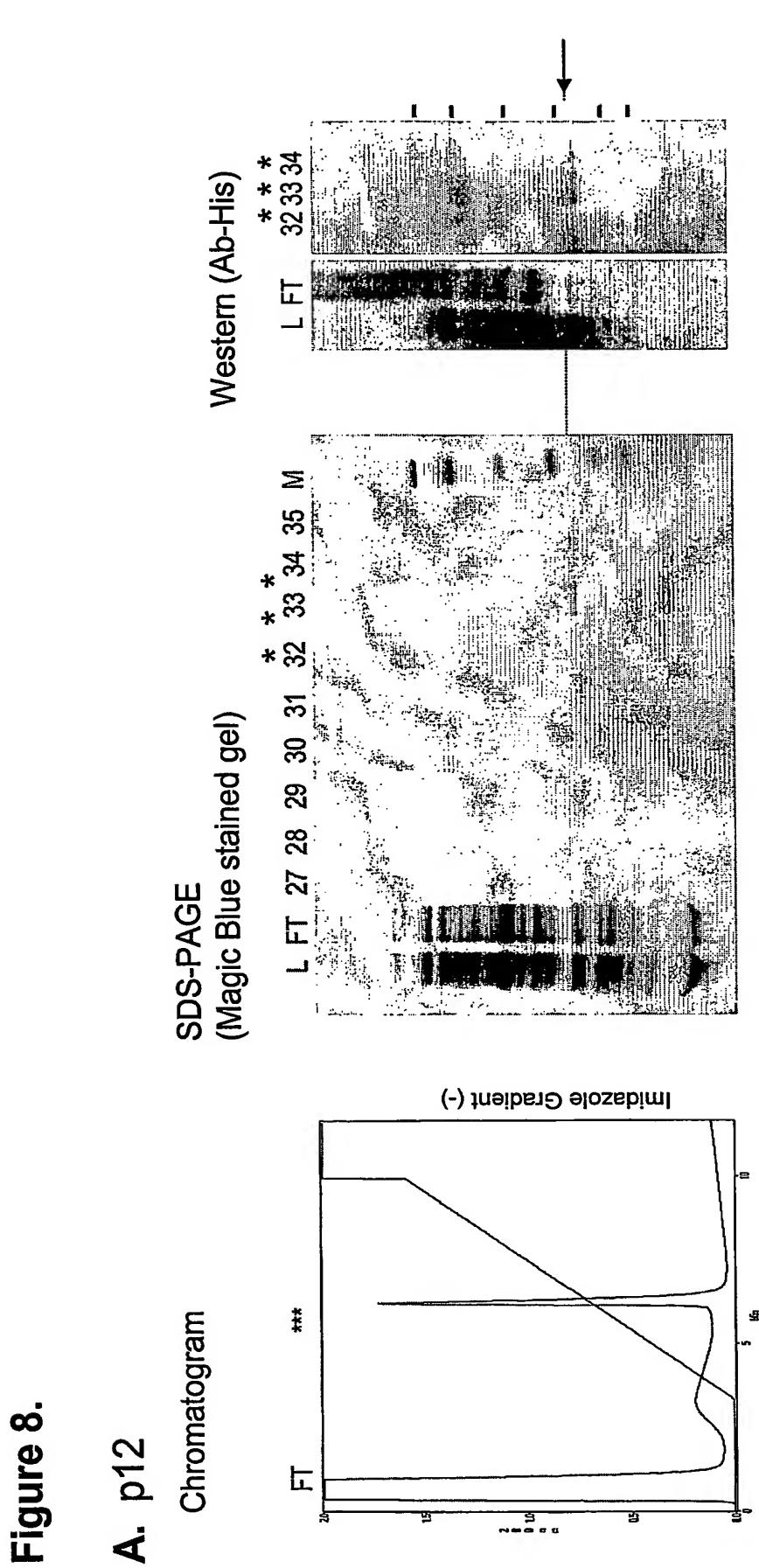
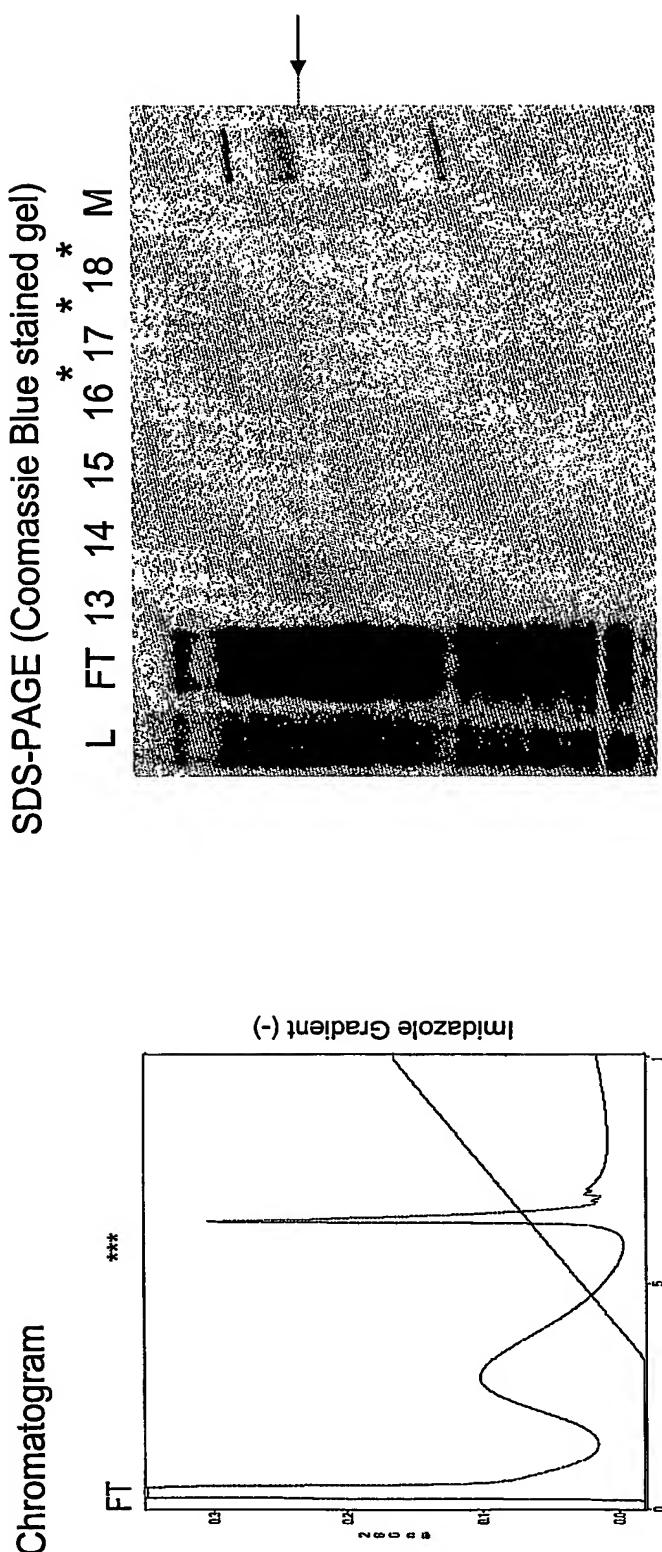
Figure 6.

Figure 7.



B. R1



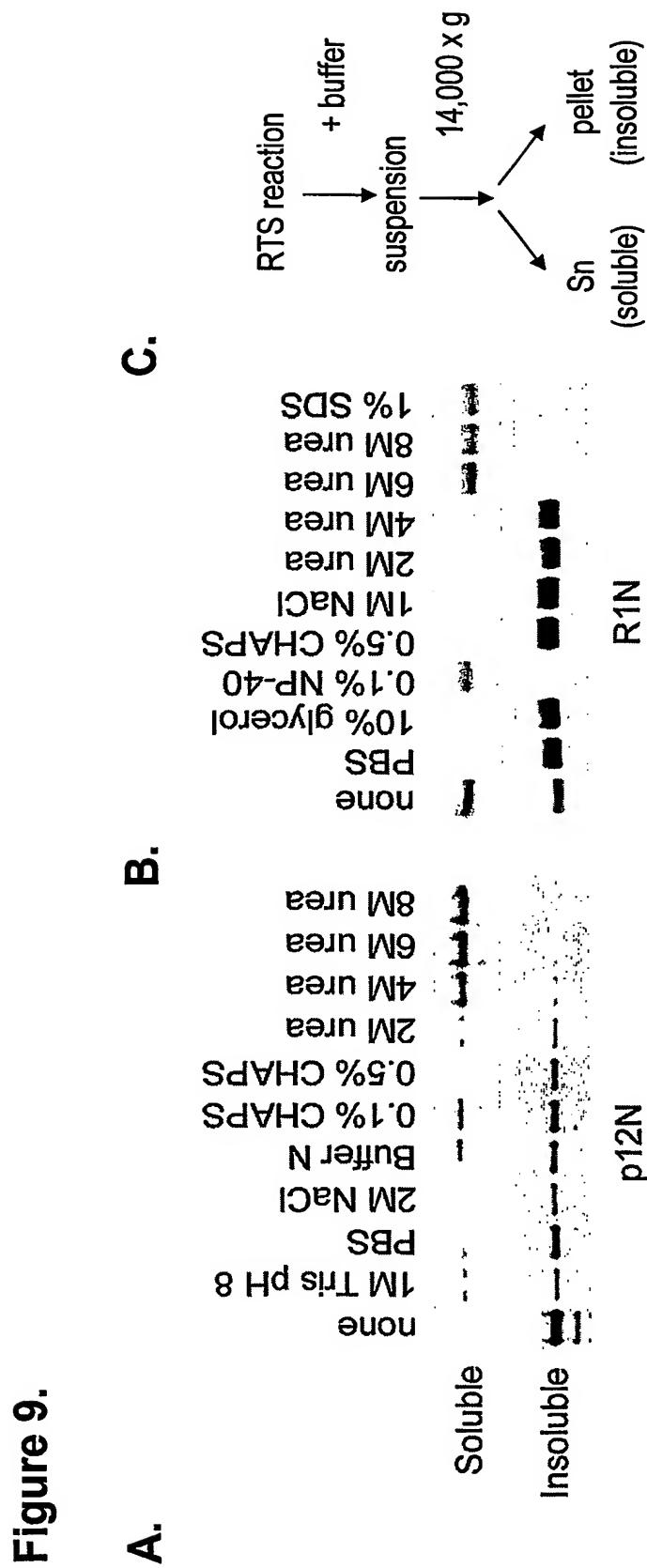
**Figure 9.**

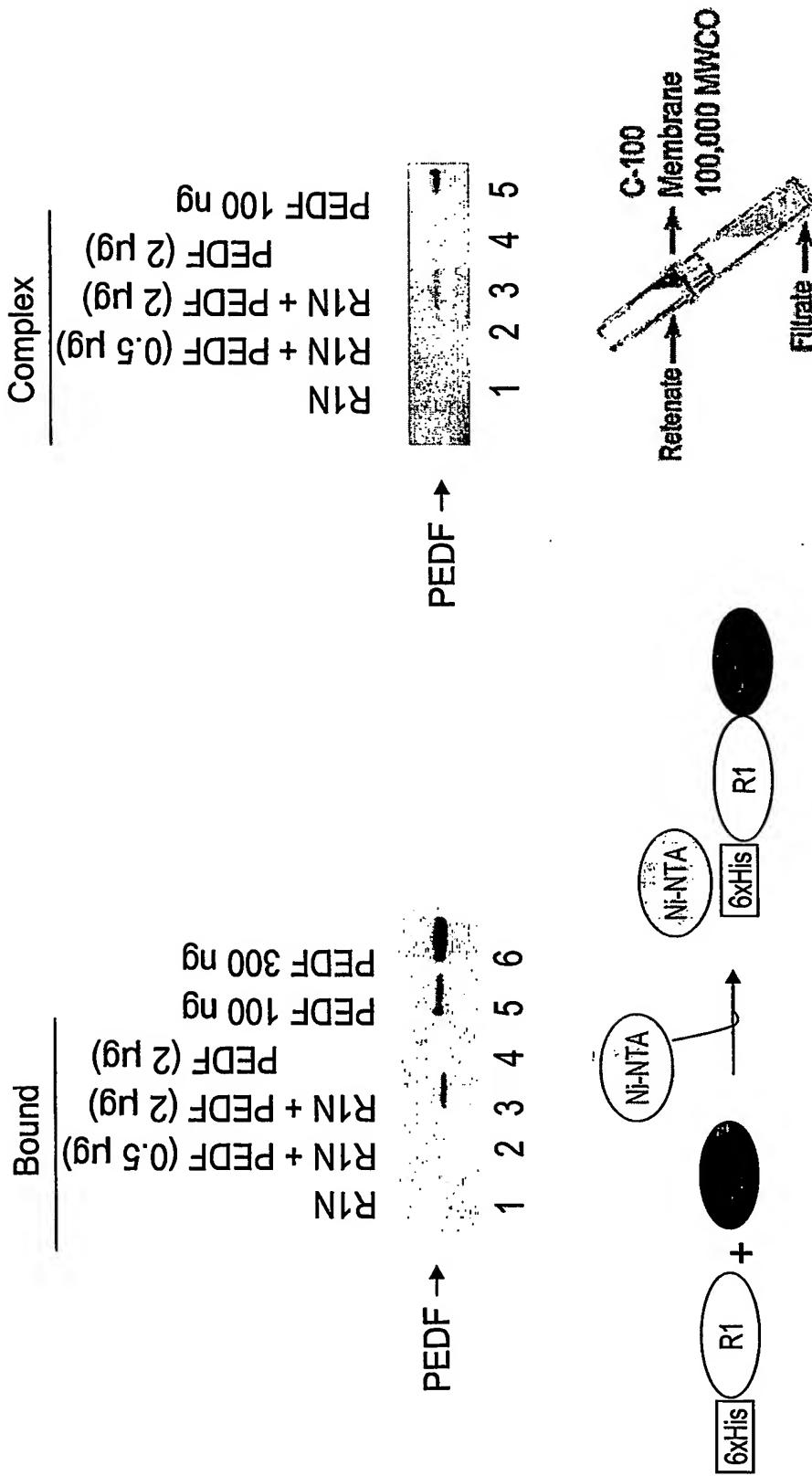
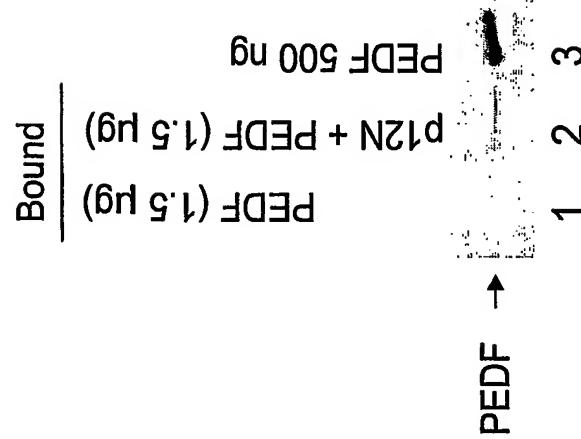
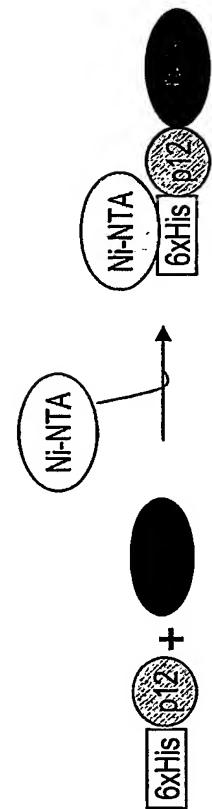
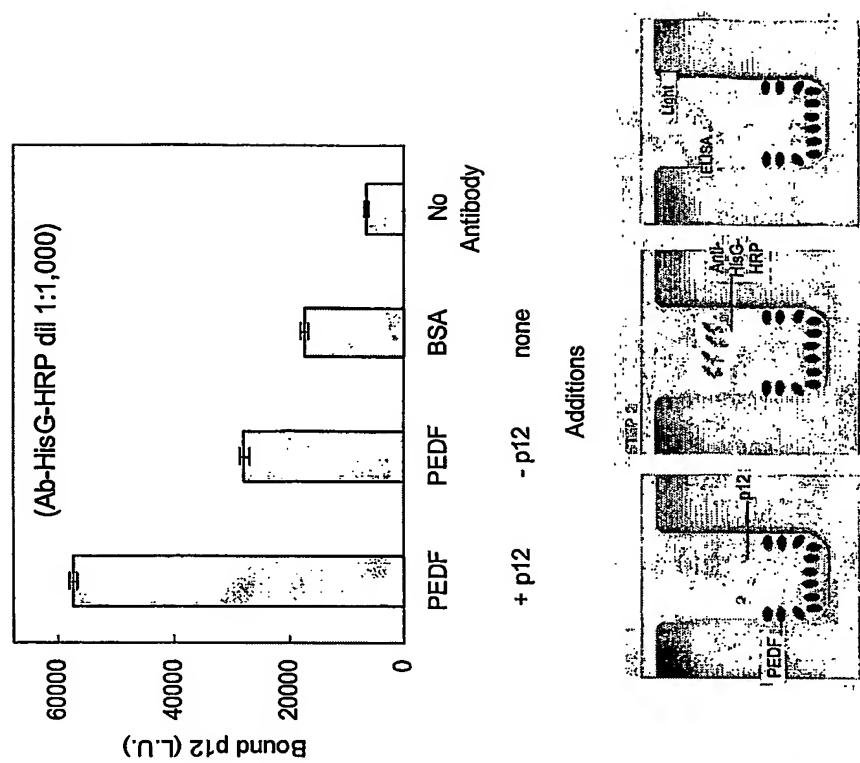
Figure 10.**A. His-tag pull-down****B. complex formation**

Figure 11.**A.****B.**

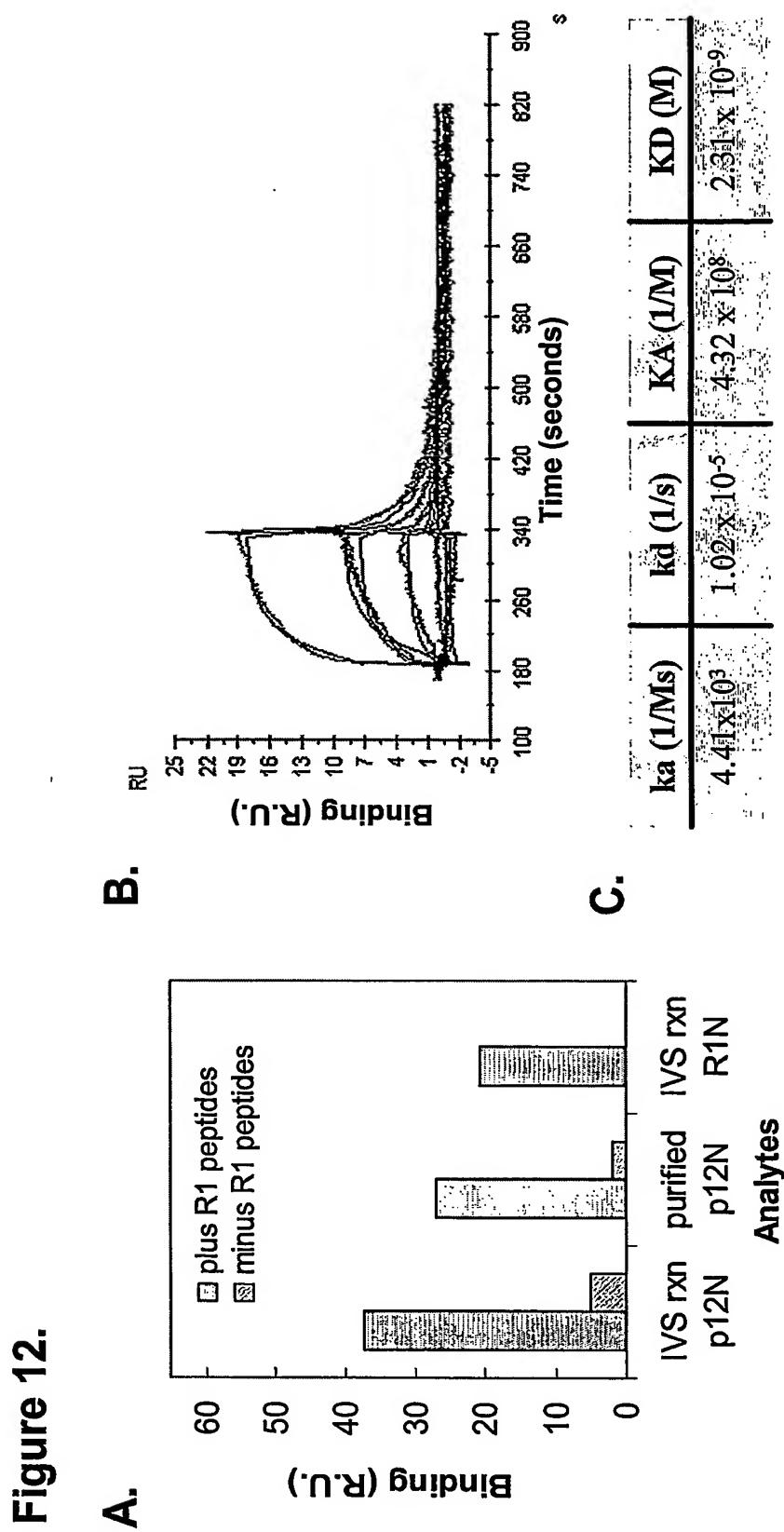


Figure 13.
A.

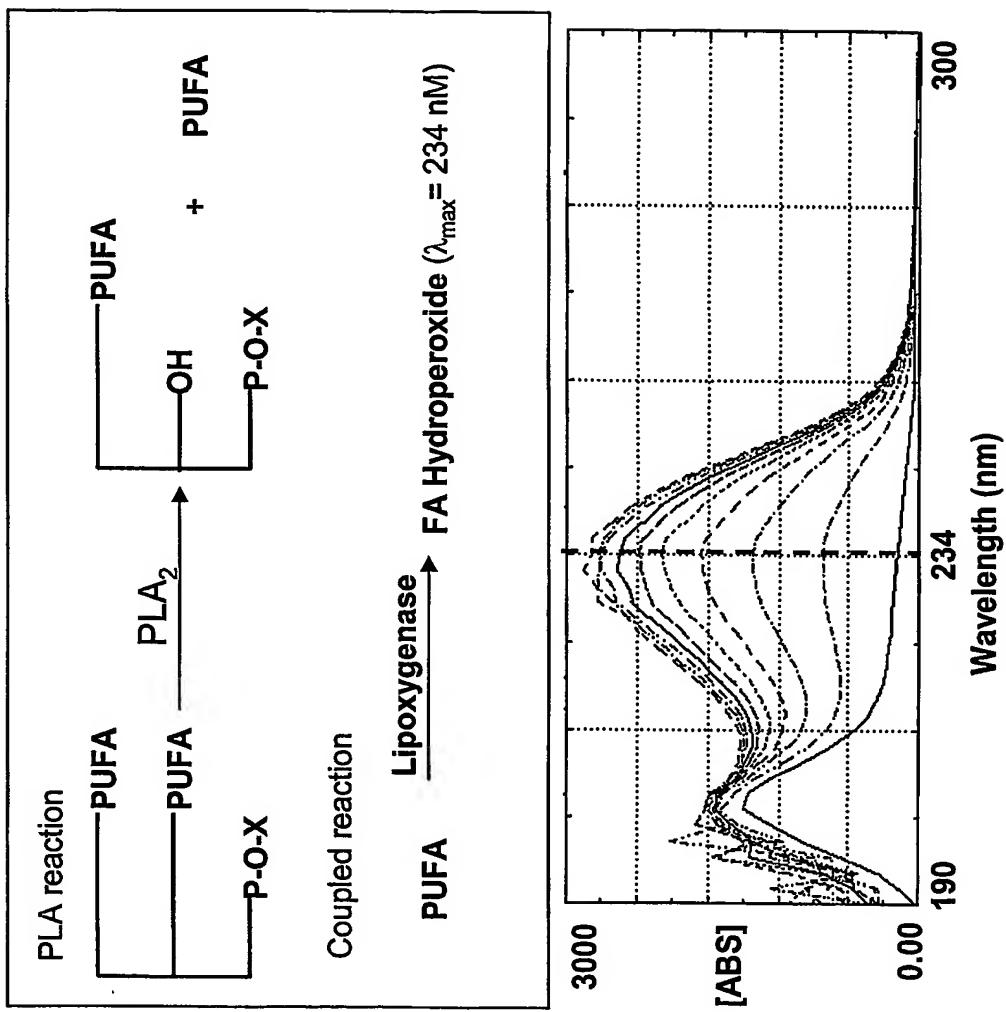
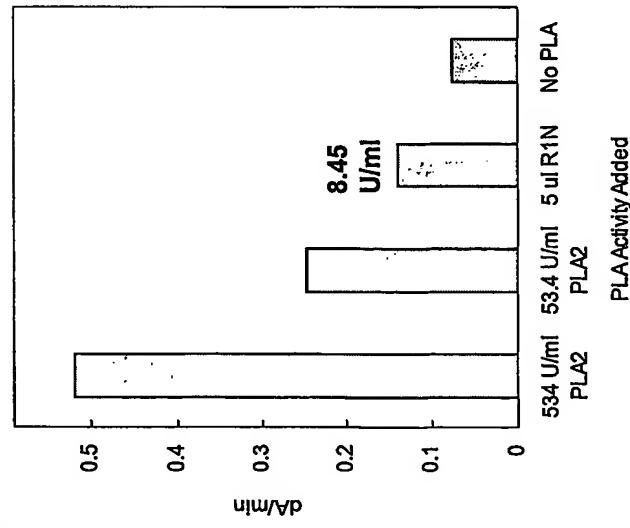
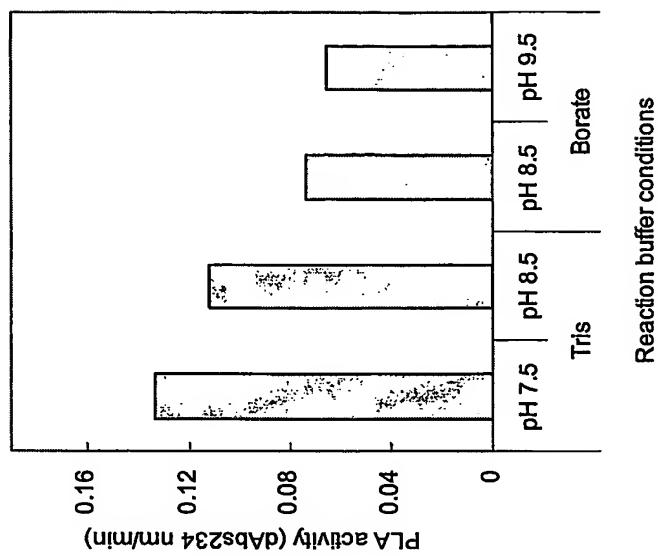


Figure 13.**B.****C.**

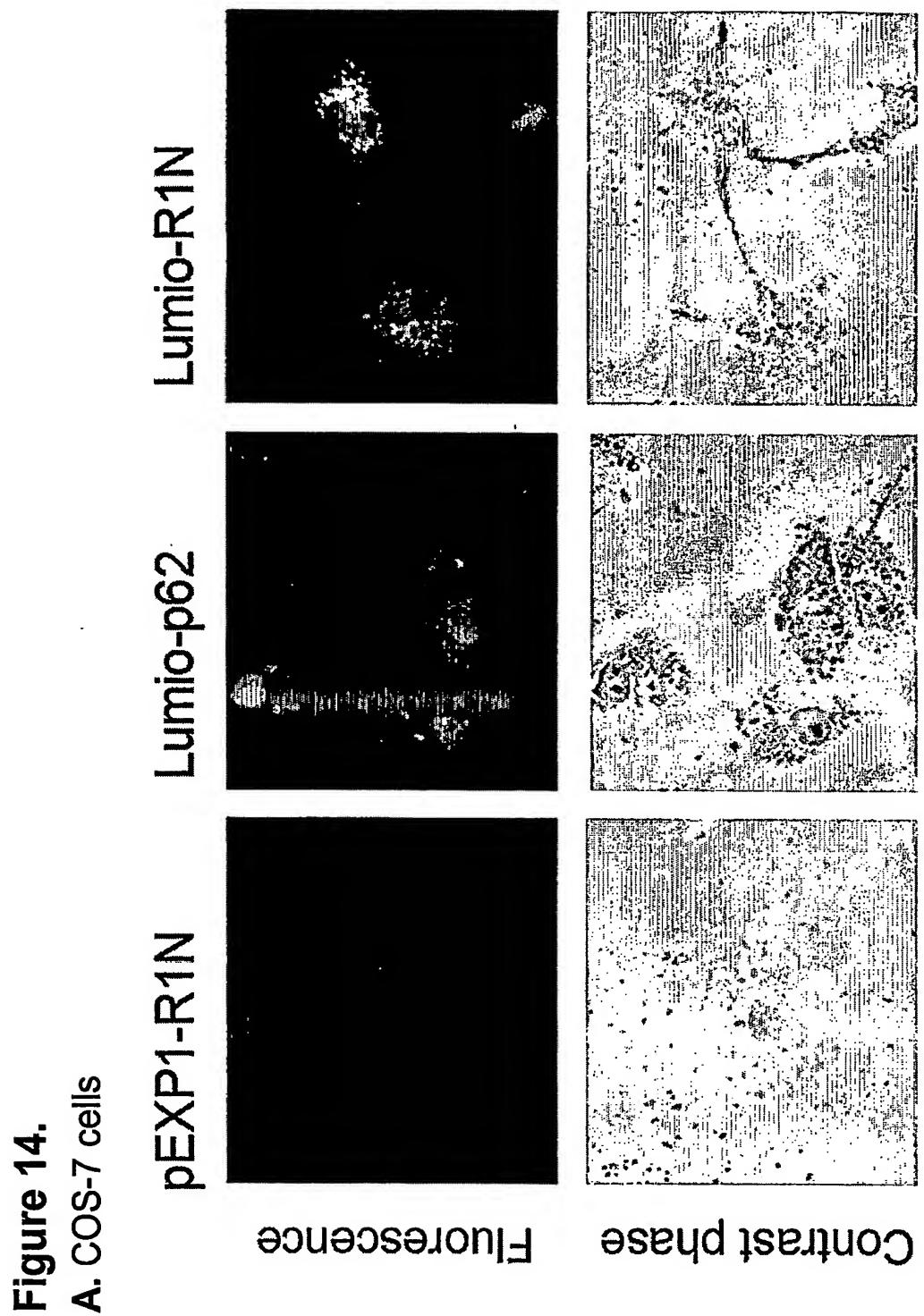


Figure 14.
B. Retinal ganglion RGC-5 cells

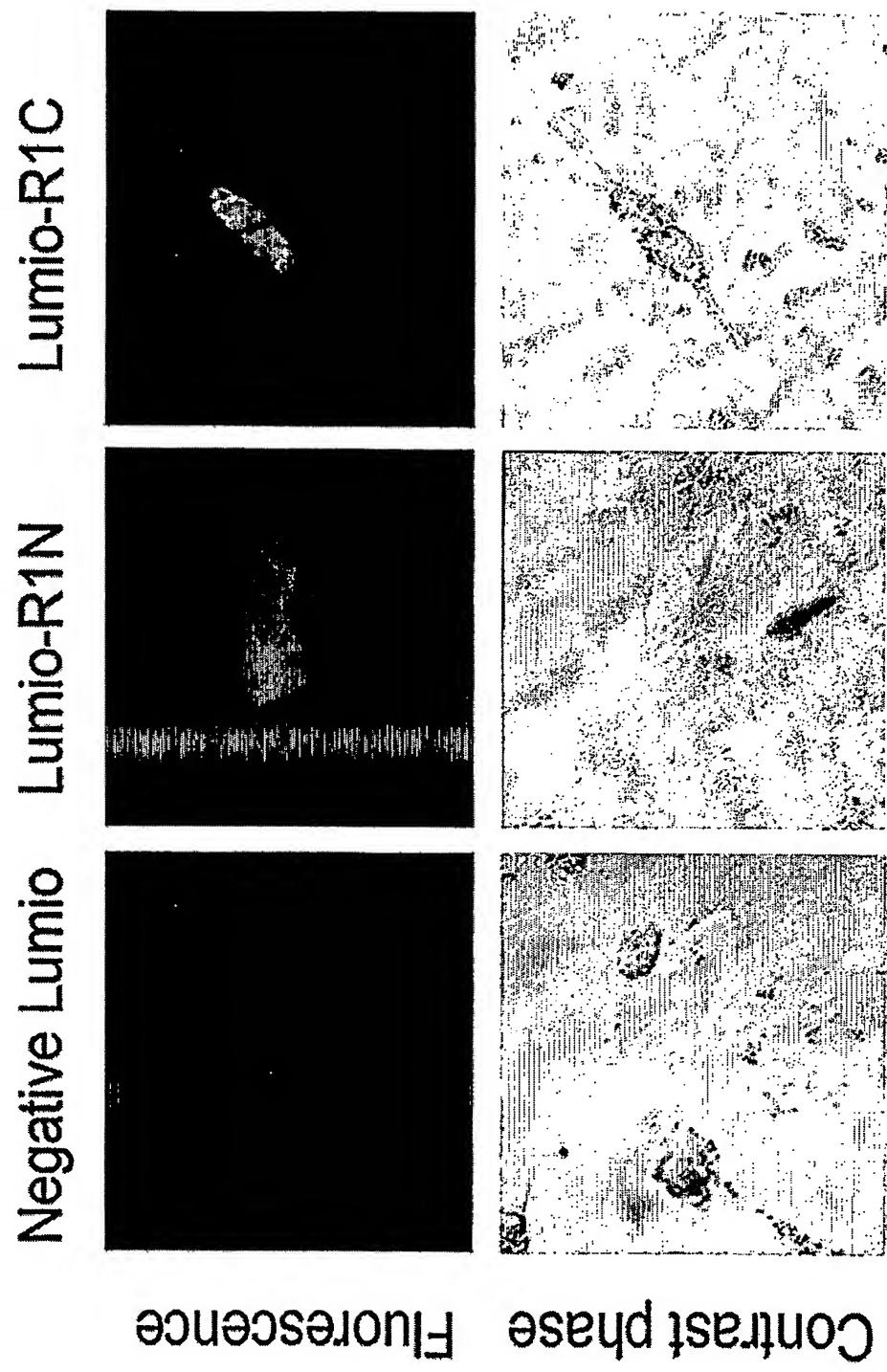
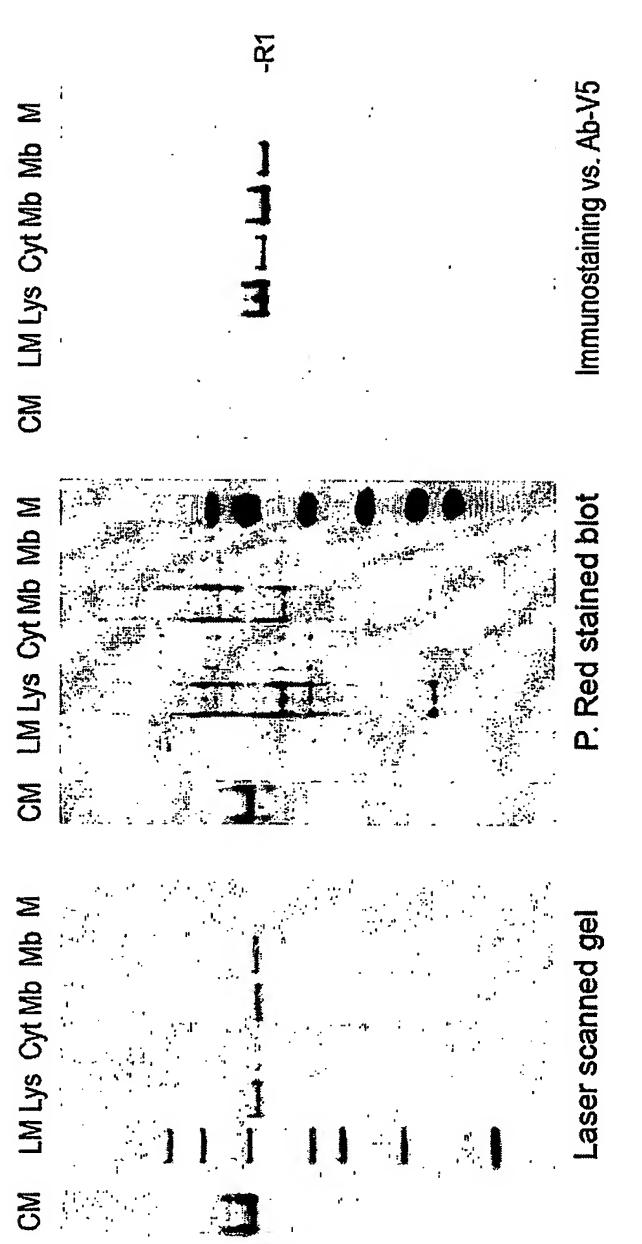


Figure 15.

LM= Lumio markers, M = MW standards CM, conditioned media; Lys, Lysate; Cyt, cytosolic; Mb, membrane fractions

Figure 16.

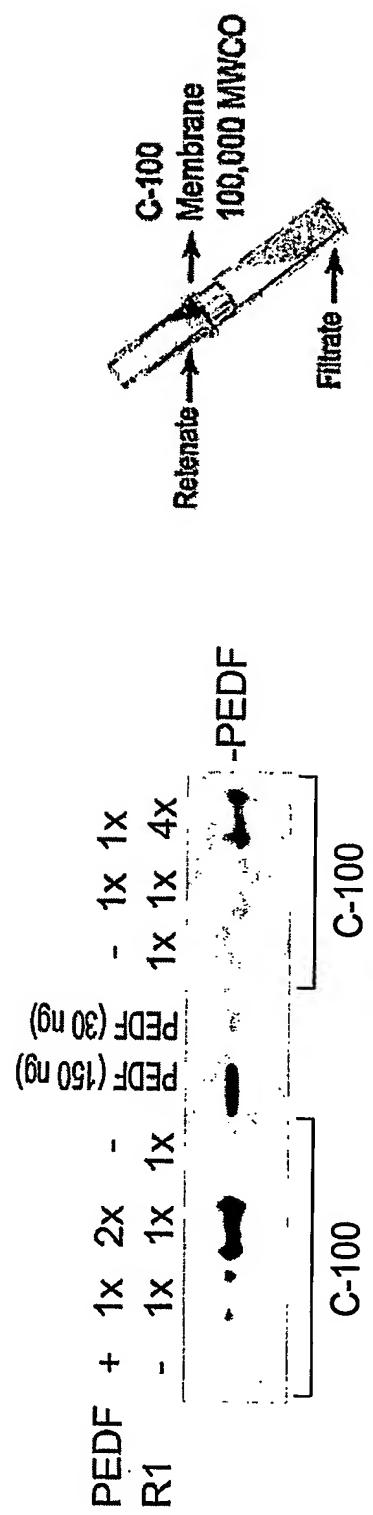


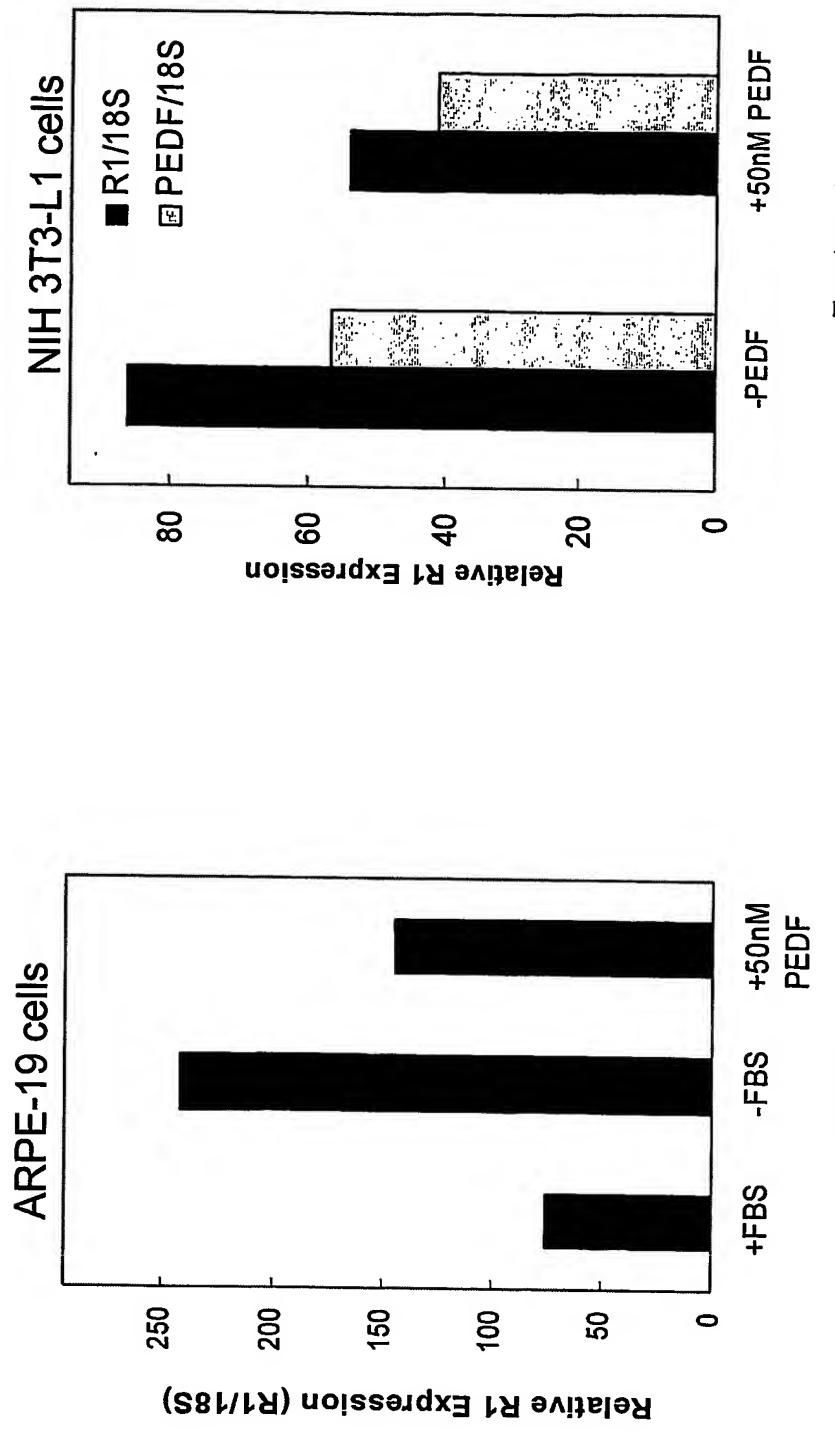
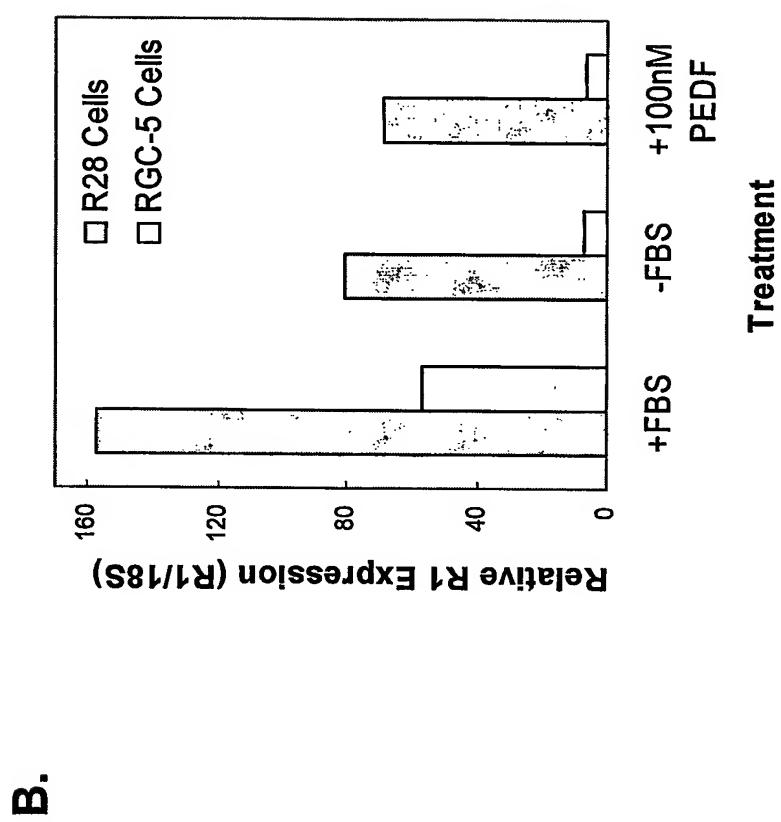
Figure 17.**A.**

Figure 17.



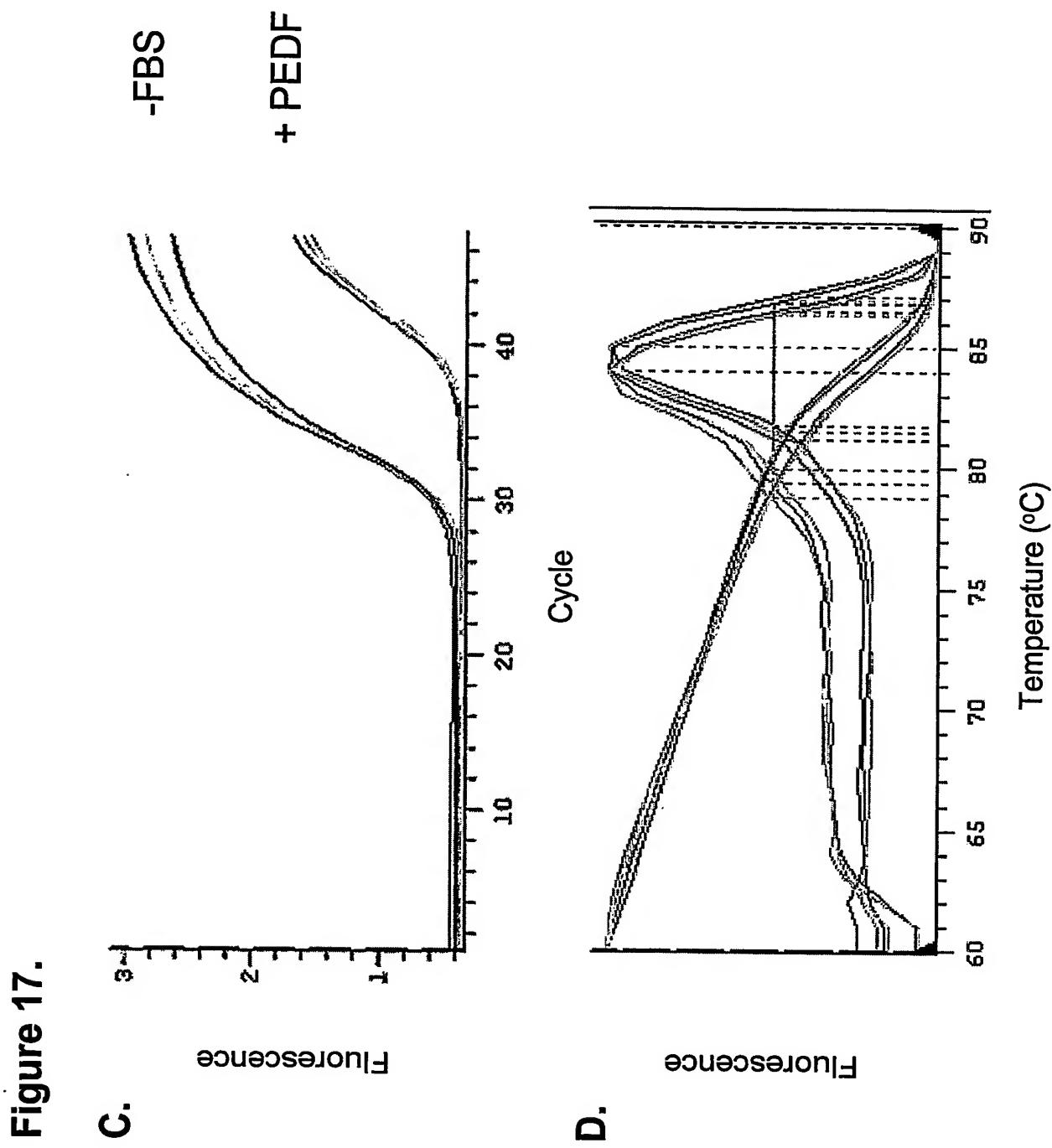


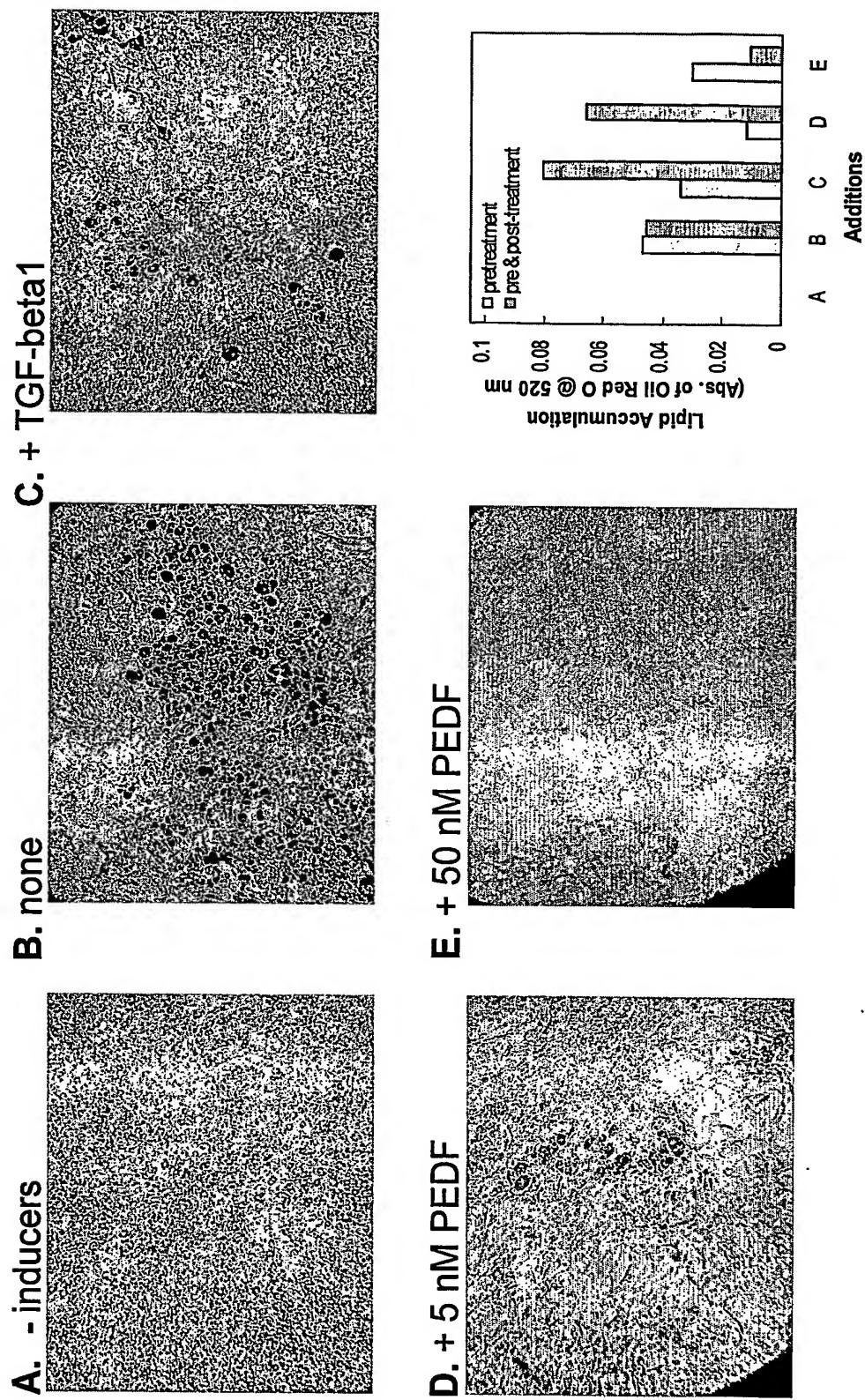
Figure 18.

Figure 19.

CLUSTAL W (1.82) multiple sequence alignment

gi|26327465|dbj|BAC27476.1| MFPRETKWNISFAGCGFLGVYHIGVASCLREHAPFLVANATHIYGASAGA 50
 gi|34861242|ref|XP_341961.1| MFPRETKWNISFAGCGFLGVYHIGVASCLREHAPFLVANATHIYGASAGA 50
 gi|16878147|gb|AAH17280.1| MFPREKTWNISFAGCGFLGVYYVGVASCLREHAPFLVANATHIYGASAGA 50
 *****.*****:*****:*****:*****:*****:*****:*****:*****:

 gi|26327465|dbj|BAC27476.1| LTATALVTGACLGEAGANIIIEVSKEARKRFLGPLHPSFNLVKTIRGCLLK 100
 gi|34861242|ref|XP_341961.1| LTATALVTGACLGEAGANIIIEVSKEARKRFLGPLHPSFNLVKTIRGCLLK 100
 gi|16878147|gb|AAH17280.1| LTATALVTGVCLGEAGAKFIEVSKEARKRFLGPLHPSFNLVKIIRSFLLK 100
 *****.*****:*****:*****:*****:*****:*****:*****:

 gi|26327465|dbj|BAC27476.1| TLPADCHERANGRLGISLTRVSDGENVIISHFSSKDELIQANVCSTFIPV 150
 gi|34861242|ref|XP_341961.1| TLPADCHTRASGRGLGISLTRVSDGENVIISHFSSKDELIQANVCSTFIPV 150
 gi|16878147|gb|AAH17280.1| VLPADSHEHASGRGLGISLTRVSDGENVIISHFN SKDELIQANVCSGFIPV 150
 .*****.*:*****:*****:*****:*****:*****:

 YCGLIPPTLQGVRYVDGGISDNLPLYLELKNTITVSPFSGESDICPQDSST 200
 YCGLIPPTLQGVRYVDGGISDNLPLYLELKNTITVSPFSGESDICPQDSST 200
 YCGLIPPSLQGVRYVDGGISDNLPLYLELKNTITVSPFSGESDICPQDSST 200
 *****:*****:*****:*****:*****:*****:

 gi|26327465|dbj|BAC27476.1| NIHELRVTNTS1QFNLRNLYRLSKALFPPEPMVLREMCKQGYRDGLRFLR 250
 gi|34861242|ref|XP_341961.1| NIHELRITNTS1QFNLRNLYRLSKALFPPEPMVLREMCKQGYRDGLRFLR 250
 gi|16878147|gb|AAH17280.1| NIHELRVTNTS1QFNLRNLYRLSKALFPPEPLVREMCKQGYRDGLRFLQ 250
 *****:*****:*****:*****:*****:

 gi|26327465|dbj|BAC27476.1| RNGLLNQPNPPLLALPPVVPQEEADAEEAAVVEERAGEEDQLQPYRKDRILE 300
 gi|34861242|ref|XP_341961.1| RNGLLNQPNPPLLALPPVVPQEEADAEEAAVTEERTGED-----RILE 292
 gi|16878147|gb|AAH17280.1| RNGLLNRPNPPLLALPPPARPHGPEDKDQAVESAQAEDYSQLP--GEDHILE 298
 *****:*****:*****:*****:*****:*****:

 gi|26327465|dbj|BAC27476.1| HLPARLNEALLEACVEPKDLMTTLSNMLPVRLATAMMV PYTLPLESAVF 350
 gi|34861242|ref|XP_341961.1| HLPARLNEALLEACVEPKDLMTTLSNMLPVRLATAMMV PYTLPLESAVF 342
 gi|16878147|gb|AAH17280.1| HLPARLNEALLEACVEPTDILTTLSNMLPVRLATAMMV PYTLPLESAVF 348
 *****:*****:*****:*****:*****:

 gi|26327465|dbj|BAC27476.1| TIRLLEWLPDV PEDIRWMKEQTGSICQYLVMRRAKRKLGDHLP SRLSEQVE 400
 gi|34861242|ref|XP_341961.1| TIRLLEWLPDV PEDIRWMKEQTGSICQYLVMRRAKRKLGDHLP SRLSEQVE 392
 gi|16878147|gb|AAH17280.1| TIRLLEWLPDV PEDIRWMKEQTGSICQYLVMRRAKRKLGRHLP SRLPEQVE 398
 *****:*****:*****:*****:*****:

 gi|26327465|dbj|BAC27476.1| LRRAQSLPSVPLSCATYSEALPNWVRNNNLSLGDALAKWEECQRQLLGLF 450
 gi|34861242|ref|XP_341961.1| LRRAQSLPSVPLSCATYSEALPNWVRNNNLSLGDALAKWEECQRQLLGLF 442
 gi|16878147|gb|AAH17280.1| LRRVQSLPSVPLSCAAAYREALPGWMRNNNLSLGDALAKWEECQRQLLGLF 448
 .**:*****:*****:*****:*****:

 gi|26327465|dbj|BAC27476.1| CTNVAFPPDALRMRAPAS--PTAADPATPQDPGGLPPC----- 486
 gi|34861242|ref|XP_341961.1| CTNVAFPPDALRMRAPAS--PTATDPATPQDPGSGLPPC----- 478
 gi|16878147|gb|AAH17280.1| CTNVAFPPPEALRMRAPADPAPAPADPASPQHQLAGPAPLLSTPAPEARPV 498
 *****:*****:*****:*****:*****:*****:

 IGALGL 504

Figure 20. (1 of 4)

CLUSTAL W (1.82) multiple sequence alignment

Figure 20. (2 of 4)

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gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01

```

TCCCCACTTAGCTCCAAGGATGAGCTCATCCAGGCCAATGTCTGCAGCAC 494
TCGCACTTAGCTCCAAGGATGAGCTTATCAGGCCAATGTTGCAGCAC 533
TCCCACCTCAACTCCAAGGACGAGCTCATCCAGGCCAATGTCTGCAGCGG 648
***** * ***** * ***** * ***** * ***** * ***** * *****

ATTATCCCGGTGTACTGTGGCCTCATTCCTACCCCTCAAGGGGTGC 544
TTTATCCCTGTGTACTGTGGCCTCATTCCTACCCCTCAAGGGGTGC 583
TTTCATCCCCGTGTACTGTGGCCTCATTCCTCCCTCCAGGGGTGC 698
***** * ***** * ***** * ***** * ***** * ***** * *****

GCTATGTGGATGGCGGCATTCAGACAACCTGCCACTTTATGAGCTGAAG 594
GCTATGTGGATGGCGGCATTCAGACAACCTGCCACTTTATGAGCTGAAG 633
GCTACCTGGATGGTGGCATTCAAGACAACCTGCCACTCTGAGCTTAAG 748
***** * ***** * ***** * ***** * ***** * ***** * *****

AATACCACATCACAGTGTCCCCATTCTCAGGCAGAGTGACATCTGCCCTCA 644
AATACCACATCACAGTGTCCCCATTCTCAGGCAGAGTGACATCTGCCACCA 683
AACACCATCACAGTGTCCCCCTCTCGGGCAGAGTGACATCTGTCCGCA 798
***** * ***** * ***** * ***** * ***** * ***** * *****

GGACAGCTCCACCAACATCCACAGGCTTCGCGTCACCAACACCAGCATCC 694
AGACAGCTCCACCAACATCCACGAACCTCGTATCACCAACACCAGCATCC 733
GGACAGCTCCACCAACATCCACGAACCTCGCAGGCTGCCACCAACACCAGCATCC 848
***** * ***** * ***** * ***** * ***** * ***** * *****

AGTCAACCTTGCACATCTTACCGCCTCTCGAAGGCTCTTCCCGCCA 744
AATTCACCTGCACATCTTACCGCCTCTCGAAGGCTCTTCCCGCCA 783
AGTCAACCTGCACATCCACCGCCTCTCGAAGGCTCTTCCCGCCG 898
***** * ***** * ***** * ***** * ***** * ***** * *****

GAGCCCATGGCTCTCCGAGAGATGTGCAAACAGGGCTACAGAGATGGACT 794
GAGCCCATGGTCTCCGAGAGATGTGCAAACAGGGCTACCGAGATGGACT 833
GAGCCCTGGTGTGCGAGAGATGTGCAAGCAGGGATACCGGGATGGCCT 948
***** * ***** * ***** * ***** * ***** * ***** * *****

TCGATCCTTAGGAGGAATGGCTACTGAACCAACCCACCCCTTGCTGG 844
TCGATCCTTAGGAGGAATGGCTACTGAACCAACCCACCCCTTGCTGG 883
GCGCTTCTGCAGGGAACGGCCTCTGAACCGGCCCCACCCCTTGCTGG 998
***** * ***** * ***** * ***** * ***** * ***** * *****

CACTGCCCCCAGTTGTCCCCCAGGAAGAGGATGCGAGGAAAGCTGCTGTG 894
CACTGCCCCCAGTTGTCCCCCAGGAAGAGGATGCGAGGAAAGCTGCCGTG 933
CGTTGCCGCCGCCCCACGG-----CCAGAGGACAAGGACAG 1042
***** * ***** * . ***** * ***** * * *

GTGGAGGAGAGGGCTGGAGAGGAGGATCAATTGCAGCCTATAGAAAAGA 944
ACTGAGGAGAGGACTGGAGGGAGGATC----- 961
GCAGTGGAGAGGCCAACGGAGGATTACTCGCAGCTGCCGGGAGAAGA 1092
***** * * * ***** * * *

TCGAATTCTAGAGCACCTGCCCTGCCAGACTCAATGAGGCCCTGCTGGAGG 994
--GGATTCTAGAGCACCTGCCCTGCCAGACTCAACGAGGCCCTGCTGGAGG 1009
TCACATCCTGGAGCACCTGCCCGCCCCGGCTCAATGAGGCCCTGCTGGAGG 1142
***** * ***** * * * * ***** * ***** * ***** * *****

CCTGTGTGGAACCAAAGGACCTGATGACCACCCCTTCCAACATGCTACCA 1044
CCTGTGTGGAACCGAAAGACCTGATGACCACCCCTTCCAACATGCTGCCA 1059
CCTGCCTGGAGGCCACGGACCTGCTGACCACCCCTCCAAACATGCTGCC 1192
***** * ***** * * * * ***** * ***** * ***** * ****

Figure 20. (3 of 4)

Figure 20. (4 of 4)

gi 26327464 dbj AK031609.1 gi 34861241 ref XM_341960.1 gi 16878146 gb BC017280.1 BC01	GTGAAACCTTCACCAAGCCACTCACTATGCTACTCCTGGTGGGGAGGGAT 1734 ----- GTGGGGCCCCCTCGCCAGCCACTCACCA-GCTGCATGCACTGAGAGGGAG 1871
gi 26327464 dbj AK031609.1 gi 34861241 ref XM_341960.1 gi 16878146 gb BC017280.1 BC01	GGGGAGTCGCCCTCCCCGGAGCCCACAGAGCCCTCCCCGTACGTC-- 1782 ----- GTTTCCACACCCCTCCCTGGGCCGCTGAGGCCCGCGCACCTGTGCCTT 1921
gi 26327464 dbj AK031609.1 gi 34861241 ref XM_341960.1 gi 16878146 gb BC017280.1 BC01	ACCTGTGCCTTACTCCTGCCACCA--CCTTTTCAGTGCAGGGTCAGTCT 1830 ----- AATCTCCCTCCCTGTGCTGCCGAGCACCTCCCCGCCCTTACTCC 1971
gi 26327464 dbj AK031609.1 gi 34861241 ref XM_341960.1 gi 16878146 gb BC017280.1 BC01	TAAGAACTCCACATCTGCTGCTGC-TCCCTGGTGTCCAAGTTCCCTTGCA 1879 ----- TGAGAACTTTGCAAGCTGCCCTCCCTCCCCGTTTCATGGCCTGCTGAA 2021
gi 26327464 dbj AK031609.1 gi 34861241 ref XM_341960.1 gi 16878146 gb BC017280.1 BC01	GA--GTGTGTGAAGAATTATTTATTTGCCAAAGCAGATCTAATAAAAG 1927 ----- ATATGTGTGTGAAGAATTATTTATTTGCCAAAGCACATGTAATAATG 2071
gi 26327464 dbj AK031609.1 gi 34861241 ref XM_341960.1 gi 16878146 gb BC017280.1 BC01	CCACAGCTCAGCTTCTGCCCTCCTCACTTCTGCATGCT----- 1965 ----- CTGCAGCCAAAAAAA A 2121
gi 26327464 dbj AK031609.1 gi 34861241 ref XM_341960.1 gi 16878146 gb BC017280.1 BC01	- - A 2122

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